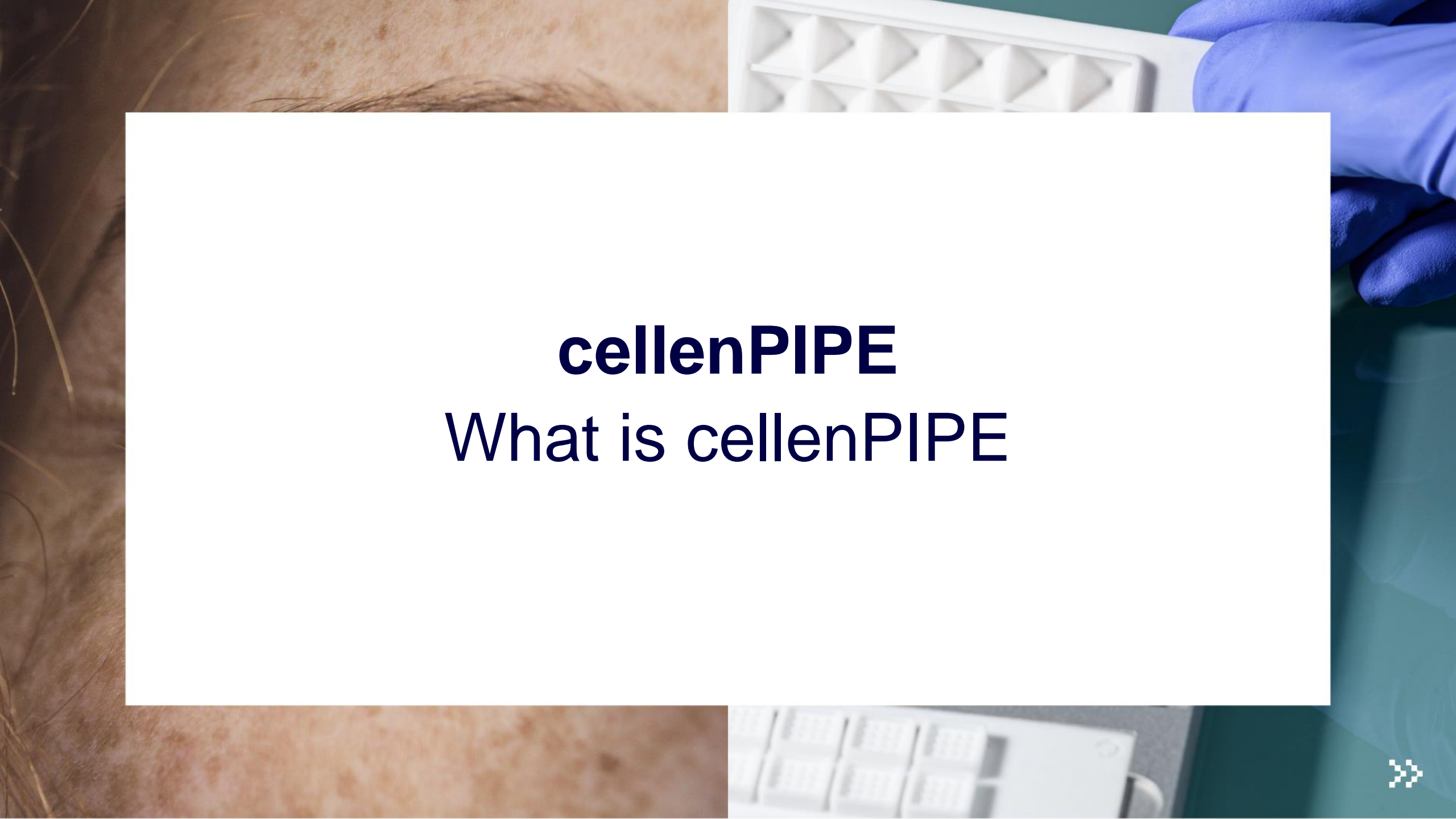


# cellenPIPE

An online single cell RNA-Seq application  
To analyze cellenCHIP kit sequencing

Authors: Robin Laffont & Laura Jarassier



# **cellenPIPE**

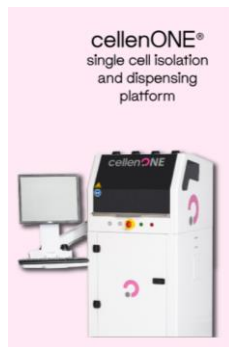
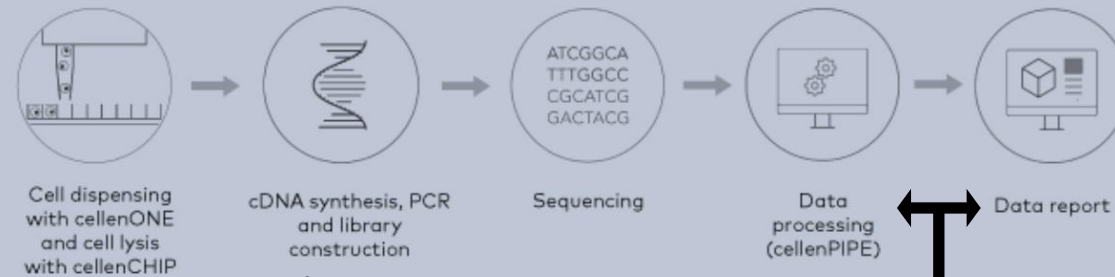
## What is cellenPIPE





# cellenPIPE: part of the cellenCHIP 384 3'RNA-Seq Kit workflow

Efficient & streamlined workflow for transcriptomic profiling of biological systems



includes

1 set of credentials w/  
3 runs per cellenCHIP  
(x4 for a kit)





# **cellenPIPE**

## The Web Application interface



# cellenPIPE: 1 set of credentials per cellenCHIP to log in...



1 set of credentials  
per cellenCHIP

**!** Required: Sequencing data from 1 cellenCHIP = 2 files for read1 & read2 FASTQ.gz format

Use cellenPIPE to run 3' single cell RNA-seq analysis - 3 runs possible per cellenCHIP 384.  
Here are the credentials for each cellenCHIP of the kit:

cellenCHIP_ID: Password:	cellenCHIP_ID: Password:
cellenCHIP_ID: Password:	cellenCHIP_ID: Password:

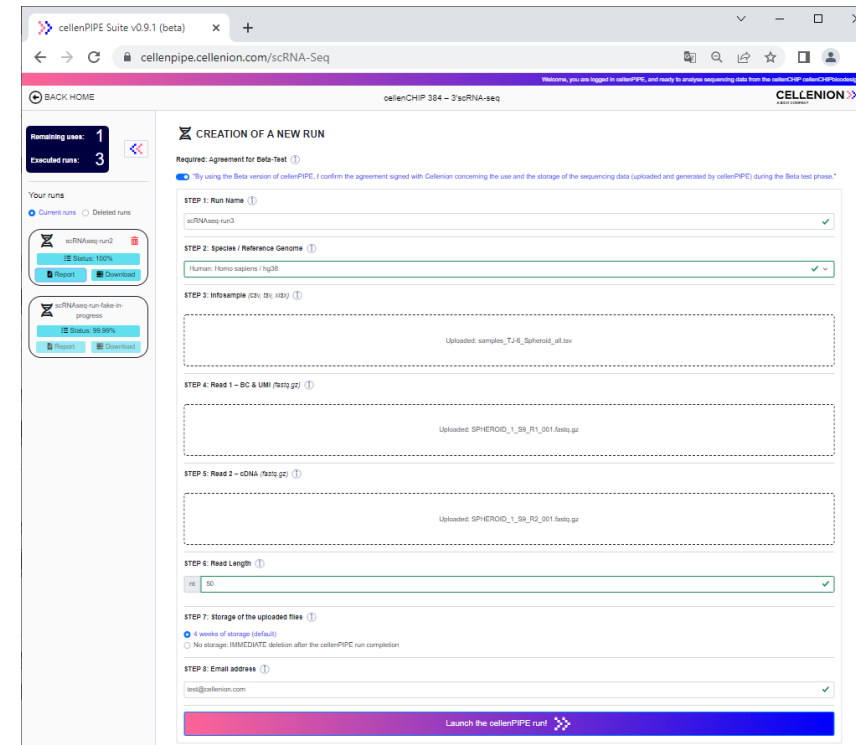
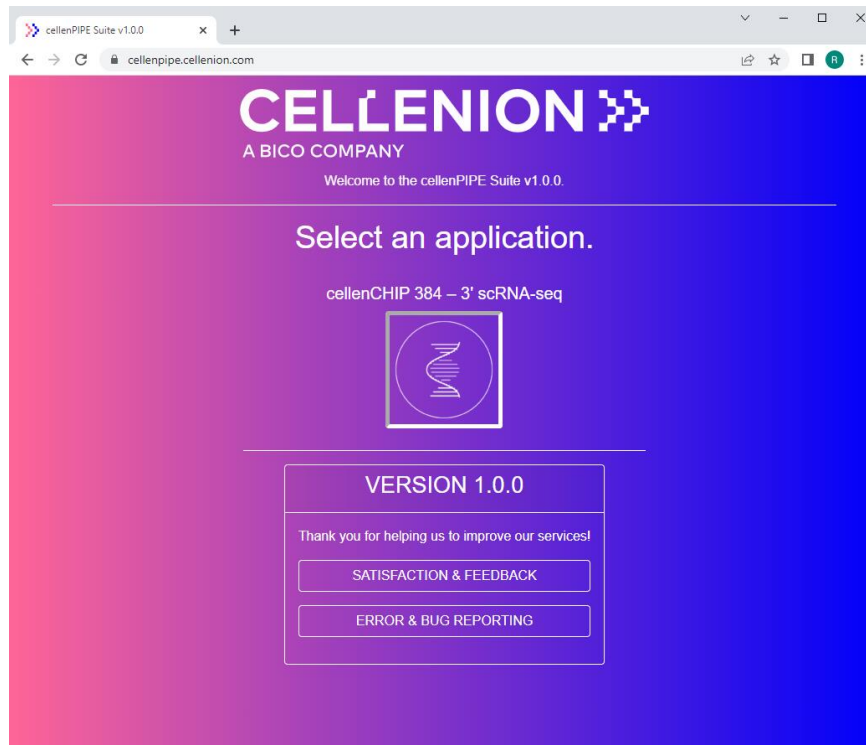
**1** Log in cellenPIPE via following address:  
[cellenpipe.cellenion.com](https://cellenpipe.cellenion.com) >>

**2** Select cellenPIPE for cellenCHIP 384-3'RNA-Seq  
cellenCHIP 384-3'RNA-Seq





cellenPIPE: ...then upload the FASTQ files, the infosample file and set the parameters of the run...



# cellenPIPE: ... launch the cellenPIPE run...

### Run Summary

Please check the following parameters:

STEP	ENTRY	STATUS
Run Name	scRNAseq-run5	✓
Species / Reference Genome	Human: Homo sapiens / hg38	✓
Infosample	samples_TJ-6_Spheroid_20.tsv	✓
BC & UMI	spheroR1_5M.fastq.gz	✓
Sequencing	spheroR2_5M.fastq.gz	✓
Read Length	cDNA: 50 nt	✓
Storage of uploaded files	4 weeks of storage	✓
Email	r.laffont@cellenion.com	✓

Number of sequenced cells: **20**  
Estimated number of reads: **3.9 million**  
Estimated duration of the cellenPIPE run: 0h 14min

Remaining uses: **1 >> 0**

Do you still want to launch this cellenPIPE run?

Let's go! ➡

Back

### cellenPIPE Progression

2022-04-26 11:21:49,069 ..... STEP 1/7: Running fastqScreen on fastq files... ✓  
2022-04-26 11:22:15,986 ...DONE in 0:00:26.924089

2022-04-26 11:22:15,986 ..... STEP 2/7: Running fastQC on fastq files... ✓  
2022-04-26 11:22:34,197 ...DONE in 0:00:18.211145

2022-04-26 11:22:34,197 ..... STEP 3/7: Running zUMIs... ✓  
2022-04-26 11:31:14,845 ...DONE in 0:08:40.648325

2022-04-26 11:31:14,845 ..... STEP 4/7: Doing some statistics... ✓  
2022-04-26 11:31:20,616 ...DONE in 0:00:05.771011

2022-04-26 11:31:20,616 ..... STEP 5/7: Running analysis by well... ■ ■ ■

Overall execution of the cellenPIPE

88.86%

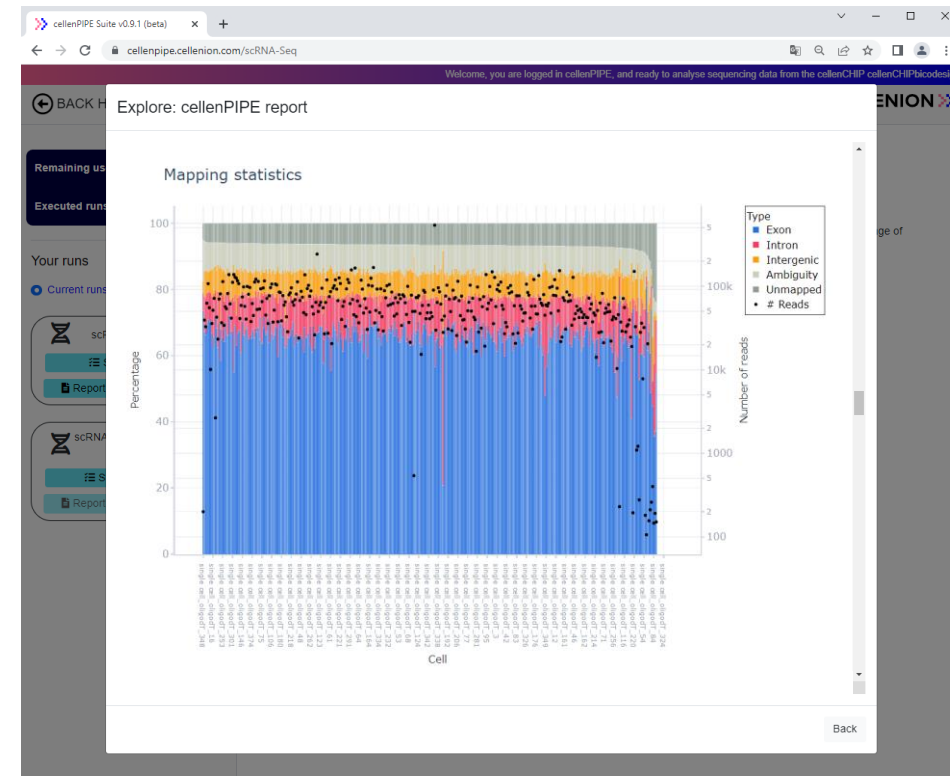
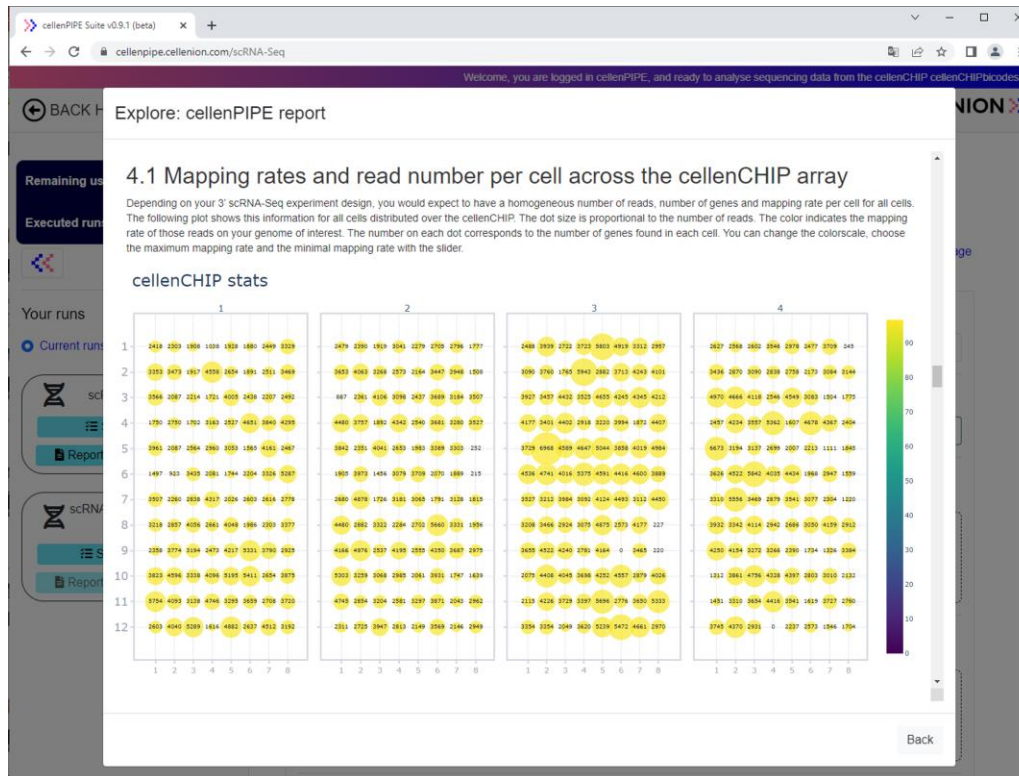
➡

You can leave the page if you want. The cellenPIPE will continue its execution. You can check the run progression in the side menu at any moment. You will also receive a confirmation mail, if indicated.

Back



# cellenPIPE: ...and finally, explore your results!





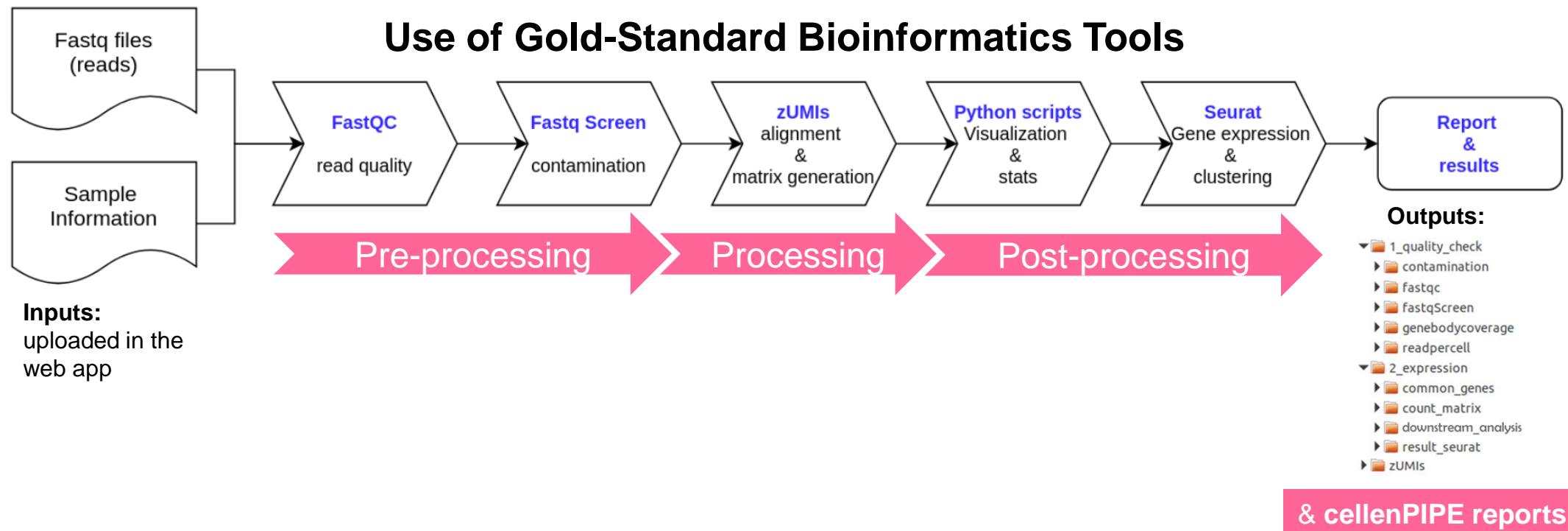


# **cellenPIPE**

**The 3' single cell RNA-seq Pipeline**



# cellenPIPE: The 3' single cell RNA-sequencing pipeline



The background of the slide is a collage of three images: a close-up of human skin on the left, a white computer keyboard in the top right, and a hand wearing a blue nitrile glove on the right side.

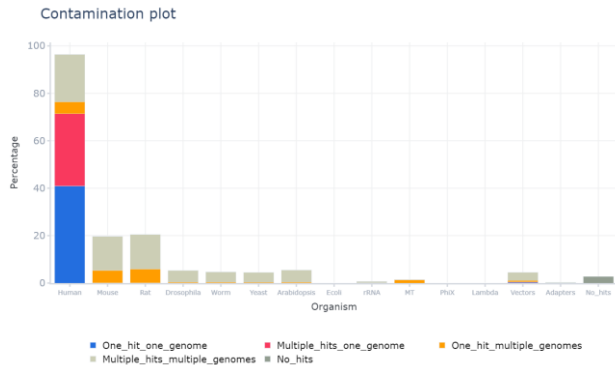
**cellenPIPE**

Results: the cellenPIPE report

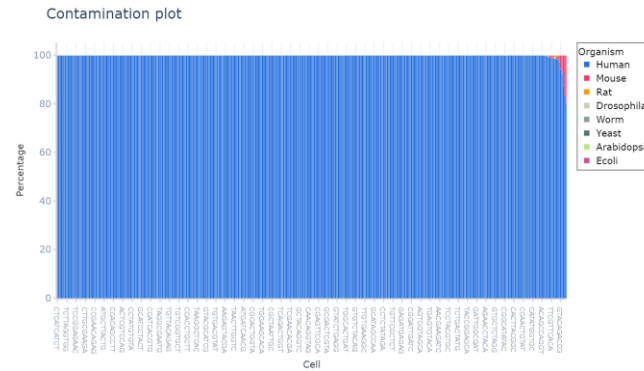




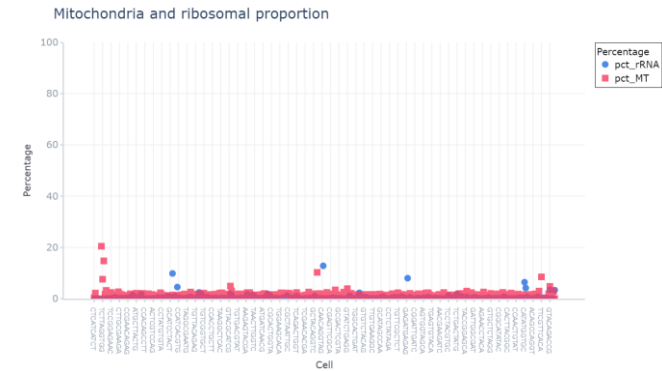
# cellenPIPE pre-processing report: Quality Control report



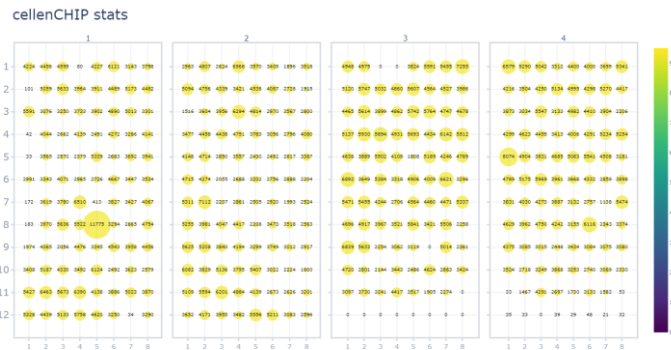
Cross-species contamination (total)



Cross-species contamination (by well)



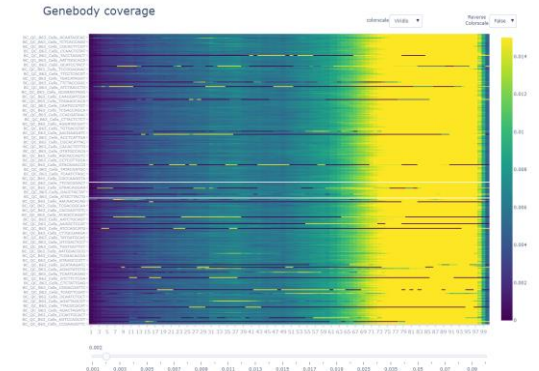
Mitochondrial & ribosomal RNA



Number of genes/reads & Mapping rates



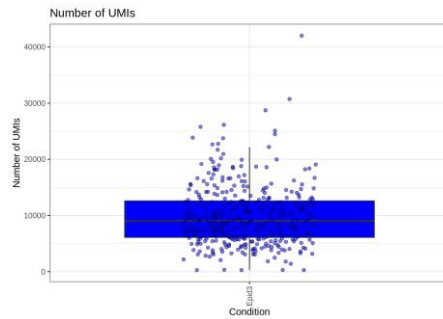
Mapping distribution



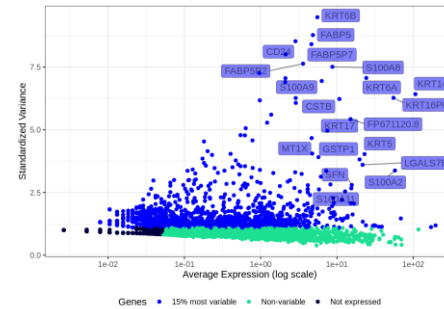
Genebody coverage



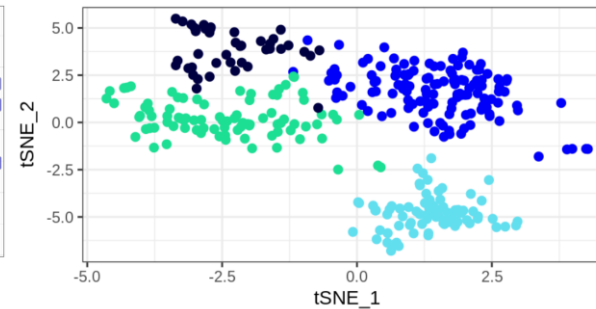
# cellenPIPE post-processing report: Exploratory analysis



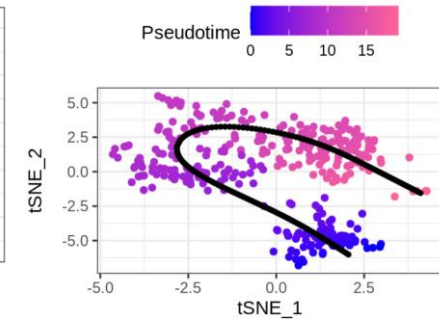
## Filtering on metrics per condition



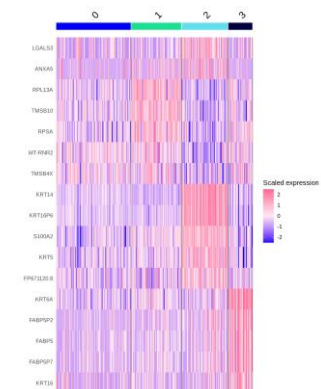
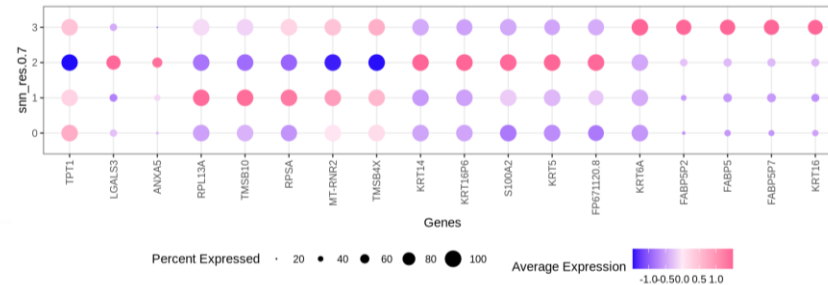
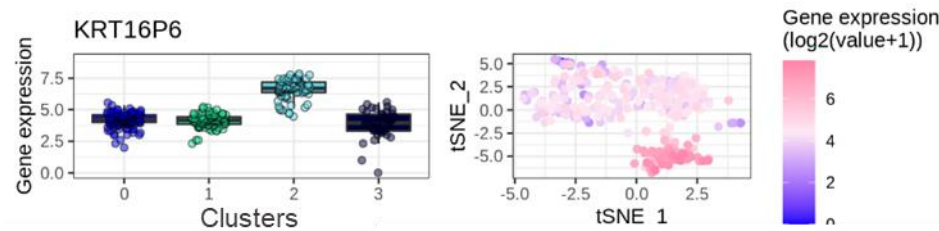
## Exploration on gene expression



## Dimension reduction & clustering



## Trajectory analysis



## Top biomarkers per cluster (boxplots, tSNE, dotplot, heatmap)

